

FIG. 1A
FIG. 1B
FIG. 1C

Top: protein produced from cDNA clone A1
Mid: protein produced from Roche patent bovine liver sequence
Bot: protein produced from Roche patent human liver sequence

FIG. 1

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SEQ ID NO: 4 MSAFRLWPGLLIMLG-SLCHRGSPCGLSTHIEIGHRALEFLQLHNGRVNYRELLLEHQDA
SEQ ID NO: 5 MSAFRFWSGLLMLLG-FLCPRSSPCGISTHIEIGHRALEFLHLQDGSINYKELLLLRHQDA
SEQ ID NO: 6 MSAFRLWPGLLMIVMASLCHRGSSCGLSTHIEIGHRALEFLHLHNGHVNYKELLLLEHQDA

YQAGIVFPDCFYPSICKGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDETEKLVAFL
YQAGSVFPDSFYPSICERGQFHDVSESTHWTPFLNASVHYIRKNYPLPWDEDETEKLVAFL
YQAGTVFPDCFYPSLCKGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDETEKLVAFL

FGITSHMAADVSWHSLGLEQQFLRTMGAIDFHGCSYSEAHSAAGDFGGDVLSEFFEFNFNYLA
FGITSHMADVNVNWHSLGIENGFLRTMAAIDFHNSYPEAHPAGDFGGDVLSEFFEFKNYLS
FGITSHMADVSWHSLGIEQQFLRTMGAIDFHGCSYSEAHSAAGDFGGDVLSEFFEFNFNYLA

FIG. 1A

RRWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLA VSKLYPTYSTKSPFL
RHWYVPAEDLLGIYRELYGRIVITKKAIVDCSYLQFLEMYAEMLAISKLYPTYSVKSPFL
RRWYVPVKDLLGIYEKLYGREVITENVIVDCSHIQFLEMYGEMLA VSKLYPSYSTKSPFL

VEQFQEYFLGGLDDMAFWSTNIYHLTSFMLENGTSDCNLPENPENPLFIACGGQQNNHTQG
VEQFQEYFLGGLDDMAFWSTNIYHLTSMLKNGTSNCNLPENP--LFTTCGGQQNNHTG
VEQFQEYFLGGLDDMAFWSTNIYHLTSFMLENGTSDCSLFENPENPLFIACGGQQNNHTQG

SKMQKNDFHRNLTTSLTESVDRNINNYTERGVFFSVNSWTPDMSFIYKALERNVRTMFIG
SKVQKNGFHKNVTAALTKNIGKHINYYTKRGVFFSVDSWTPDMSFMYKSLESI REMFIG
SKMQKNDFHRNLTTSLTENIDRNINNYTERGVFFSVNSWTPDMSFIYKALERNVRTMFIG

GSQLSQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGRIHIGRV
SSQP-LTHVSSPAASYLSFPYTRLGWAMTSADLNQDGYGDLVVGAPGYSHPGRIHVGRV
GSQLSQKHISSPLASYFLSFPYARLGWAMTSADLNQDGYGDLVVGAPGYSRPGRIHIGRV

YLIYGNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLD FNVDPDLAVGAPSVGS
YLIYGNDLG-PRIDLDDKEAHGILEGFQPSGRFGSAVAVLD FNVDPDLAVGAPSVGS
YLIYGNELGLPPVDLDDKEAHGILEGFQPSGRFGSALAMLD FNMMDGVPDLAVGAPSVGS

EQLTYKGAVYVYFGSKQGMSSSPNITISCQDIYCNLGWTL LAAADVNGDSEPD-LVIGSP
EKLTYTGAVYVYFGSKQQLSSSPNVTISCQDIYCNLGWTL LAAADVNGDSEPD L FVIGSP
EQLTYKGAVYVYFGSKQGRMSSSPNITISCQDIYCNLGWTL LAAADVNGDSEPD-LVIGSP

FIG. 1B

FAPGGKQKGI VAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLL
 FAFGGKQKGI VAAFYSGSSYSREKLNVEAANWVMVKEEDFAWLGYSLHGVNVNRTLL
 FAPGGKQKGI VAAFYSGPSLSNKEKLNVEAANWTVRGEEDFAWFGYSLHGVTVDNRTLL

LVGSPTWKNASRLGHLHIRDEKKS LGRVGYFPPNGQSWFTISGDKAMKLGTSLS SGH
 LAGSPTWKDTSSQGH LFRTRDEKQSPGRVGYFPPI CQSWFTISGDKAMKLGTSLS SGH
 LVGSPTWKNASRLGRLHIRDEKKS LGRVGYFPPNSQSWFTIVGDKAMKLGTSLS SGH

VLMNGTLKQVLLVGAPTYDDVSKVAFLTVTLHQGGATRMVALISDAQPLLLSTFSGDRRF
 VIVNGTRTQVLLVGAPTQDVVSKS - FLTMTLHQGGSTRMYELTPDSQPSLLSTFSGNRRF
 VLMNGTLTQVLLVGAPTRDDVSKMAFLTMTLHQGGATRMVALTSDLQPPLLSTFSGDRRF

SRFGGVLHLSDDLDDGLDEI IMAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKC
 SRFGGVLHLSDDLNDGLDEI IVAAPLRIADTAGLMGEEDGRVYVFNGKQITVGDVTGKC
 SRFGGVLHLSDDLDDGVDEI IVAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKC

KSWITPCPEEKAQYVLISPEASSRFGSSLI TVRSKAKNQVIAAGRSSLGARLSGALHVY
 KSWVTPCPEEKAQYVLISPEAGSRFGSSVITVRSKEKNQVIAAGRSSLGARLSGVLHIY
 KSWMTPCPEEKAQYVLISPEASSRFGSSLI TVRSKAKNQVIAAGRSSLGARLSGALHVY

SLGSD
 RLQD
 SLGSD

FIG. 1C

FIG. 2A
FIG. 2B
FIG. 2C
FIG. 2D
FIG. 2E
FIG. 2F
FIG. 2G
FIG. 2H
FIG. 2I
FIG. 2J
FIG. 2K

FIG. 2

Top: pancreatic-form cDNA sequence from GenBank database SEQ ID NO: 7
mid: our sequence cloned from human liver cDNA library SEQ ID NO: 8
bot: Roche patent pancreatic-form partial cDNA sequence SEQ ID NO: 9

1	GTGACCTGCTTAGAGAGAAAGCGGTGGTCTGCACCTGGATTTTGGAGTCCCAGTGCTGCT	60

1	-----ATGTCTGCT	9
61	GCAGCTCTGAGCATTTCCACGTCAACAGAGAAAGCCGGTGGGCAATGAGAGCATGTCTGCT	120

FIG. 2A

10 TTCAGGTTGTGGCCTGGCCCTGCTGATCATGTTGGGTTCTCTCTGCCATAGAGGTTCAACG 69
121 TTCAGGTTGTGGCCTGGCCCTGCTGATCATGTTGGGTTCTCTCTGCCATAGAGGTTCAACG 180

70 TGTGGCCTTTCAACACACACGTAGAAATAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 129
181 TGTGGCCTTTCAACACACACATAGAAATAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 240

130 AATGGGCGTGTTAACTACAGAGAGCTGTACTAGAACACACAGGATGCGTATCAGGCTGGA 189
241 AATGGGCGTGTTAACTACAGAGAGCTGTACTAGAACACACAGGATGCGTATCAGGCTGGA 300

190 ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAGAGGAGGAAAATTCCATGATGTG 249
301 ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAGAGGAGGAAAATTCCATGATGTG 360

250 TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC 309
361 TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC 420

FIG. 2B

310 TATCCCCCTTCCCTGGGAGAAGGACACAGAGAAACTGGTAGCTTTCCTTGTGGAATTACT 369
421 TATCCCCCTTCCCTGGGAGAAGGACACAGAGAAACTGGTAGCTTTCCTTGTGGAATTACT 480

370 TCTCACATGGCGGCAGATGTCAGCTGGCATACTCTGGGCCCTTGAAACAAGGATTCCTTAGG 429
481 TCTCACATGGCGGCAGATGTCAGCTGGCATACTCTGGGCCCTTGAAACAAGGATTCCTTAGG 540

430 ACCATGGGAGCTATTGATTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 489
541 ACCATGGGAGCTATTGATTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 600

490 GGAGGAGATGTGTGAGCCAGTTTGAAATTTAATTTAATTACCTTGACACGACGCTGGTAT 549
601 GGAGGAGATGTGTGAGCCAGTTTGAAATTTAATTTAATTACCTTGACACGACGCTGGTAT 660

550 GTGCCAGTCAAAGATCTACTGGGAATTTATGAGAAACTGTATGGTCGAAAAGTCATCACC 609
661 GTGCCAGTCAAAGATCTACTGGGAATTTATGAGAAACTGTATGGTCGAAAAGTCATCACC 720

610	GAAAATGTAATCGTTGATTGTTCA	669
721	GAAAATGTAATCGTTGATTGTTCA	780

670	GCTGTTTCCAAAGTTATATCCCACT	729
781	GCTGTTTCCAAAGTTATATCCCACT	840

730	CAAGAGTATTTTCTTGGAGGACTGG	789
841	CAAGAGTATTTTCTTGGAGGACTGG	900

790	CTAACAAATCTTCATGTTGGAGAA	849
901	CTAACAAAGCTTTCATGTTGGAGAA	960

850	TTCAATTGCATGTGGCGGCCAGCAA	909
961	TTCAATTGCATGTGGCGGCCAGCAA	1020

910	TTTCACAGAAATTTGACTACATCCCT	969
1021	TTTCACAGAAATTTGACTACATCCCT	1080

970 GAAAGAGGAGTGTCTTTAGTGTAATTCCTGGACCCCGGATTCCATGTCCTTTATCTAC 1029
1081 GAAAGAGGAGTGTCTTTAGTGTAATTCCTGGACCCCGGATTCCATGTCCTTTATCTAC 1140

1030 AAGGCTTTGGAAAGGAACATAAGGACAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1089
1141 AAGGCTTTGGAAAGGAACATAAGGACAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1200

1090 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCAATTTCCCTTATGCGAGGCTTGGCTGG 1149
1201 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCAATTTCCCTTATGCGAGGCTTGGCTGG 1260

1150 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGTGGGCGCACCA 1209
1261 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGTGGGCGCACCA 1320

1210 GGCTACAGCCGCCCGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1269
1321 GGCTACAGCCGCCCGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1380

1270 CTGGGCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCACAGGATCCTTGAAGGC 1329
1381 CTGGGCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCACAGGATCCTTGAAGGC 1440

FIG. 2E

1330 TTCAGCCCTCAGGTCGGTTTGGCTCGGCCTTGGCTGTGTGGACTTTAACGTGGACGGC 1389
1441 TTCAGCCCTCAGGTCGGTTTGGCTCGGCCTTGGCTGTGTGGACTTTAACGTGGACGGC 1500

1390 GTGCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1449
1501 GTGCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1560

1450 GCCGTGTATGTCTACTTTGGTTCCAAACAAGGAGGAATGTCTTCTTCCCCTAACATCACC 1509
1561 GCCGTGTATGTCTACTTTGGTTCCAAACAAGGAGGAATGTCTTCTTCCCCTAACATCACC 1620

1510 ATTTCTTGCCAGGACATCTACTGTAACTTGGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1569
1621 ATTTCTTGCCAGGACATCTACTGTAACTTGGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1680

1570 GGAGACAGTGAACCCGATCTGGTCATCGGCTCCCTTTTGCACCAGGTGGAGGGAAGCAG 1629
1681 GGAGACAGTGAACCCGATCTGTGTATCGGCTCCCTTTTGCACCAGGTGGAGGGAAGCAG 1740

1630 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 1689
1741 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 1800
1 -----CTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 35

FIG. 2F

1690 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 1749
1801 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 1860
36 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 95

1750 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTTGGTGGAGCCCGACCTGGAAG 1809
1861 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTTGGTGGAGCCCGACCTGGAAG 1920
96 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTTGGTGGAGCCCGACCTGGAAG 155

1810 AATGCCAGCAGGCTGGGCCATTGTGTTACACATCCGAGATGAGAAAAGAGCCTTGGGAGG 1869
1921 AATGCCAGCAGGCTGGGCCATTGTGTTACACATCCGAGATGAGAAAAGAGCCTTGGGAGG 1980
156 AATGCCAGCAGGCTGGGCCATTGTGTTACACATCCGAGATGAGAAAAGAGCCTTGGGAGG 215

1870 GTGTATGGCTACTTCCCACCAAACGGCCAAAGCTGGTTTACCATTCTGGAGACAAGGCA 1929
1981 GTGTATGGCTACTTCCCACCAAACGGCCAAAGCTGGTTTACCATTCTGGAGACAAGGCA 2040
216 GTGTATGGCTACTTCC - ACCAAACGGCCAAAGCTGGTTTACCATTCTGGAGACAAGGCA 275

1930 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTA CTGATGAATGGGACTCTGAAA 1989
2041 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTA CTGATGAATGGGACTCTGAAA 2100
276 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGTCACGTA CTGATGAATGGGACTCTGAAA 335

1990 CAAGTGCTGCTGTTGGAGCCCCCTACGTACGATGACGTGCTAAGGTGGCATTCCTGACC 2049
2101 CAAGTGCTGCTGTTGGAGCCCCCTACGTACGATGACGTGCTAAGGTGGCATTCCTGACC 2160
336 CAAGTGCTGCTGTTGGAGCCCCCTACGTACGATGACGTGCTAAGGTGGCATTCCTGACC 395

FIG. 2G

2050 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATATCTGACGCGCAGCCT 2109
2161 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATATCTGACGCGCAGCCT 2220
396 GTGACCCCTACACCAAGGCGGAGCCACTCGCGTGTACGCACTCATATATCTGACGCGCAGCCT 455

2110 CTGCTGCTCAGCACCTTCAGCGGAGACCGCGCTTCTCCGATTTGGTGGCGTTCTGCAC 2169
2221 CTGCTGCTCAGCACCTTCAGCGGAGACCGCGCTTCTCCGATTTGGTGGCGTTCTGCAC 2280
456 CTGCTGCTCAGCACCTTCAGCGGAGACCGCGCTTCTCCGATTTGGTGGCGTTCTGCAC 515

2170 TTGAGTGACCTGGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 2229
2281 TTGAGTGACCTGGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 2340
516 TTGAGTGACCTGGATGATGGCTTAGATGAAATCATCATGGCAGCCCCCTGAGGATA 575

2230 GCAGATGTAACCTCTGGACTGATTGGGGAGAAAGACGGCCGAGTATATGTATATAATGGC 2289
2341 GCAGATGTAACCTCTGGACTGATTGGGGAGAAAGACGGCCGAGTATATGTATATAATGGC 2400
576 GCAGATGTAACCTCTGGACTGATTGGGGAGAAAGACGGCCGAGTATATGTATATAATGGC 635

2290 AAAGAGACCAACCCTTGGTGACATGACTGGCAAATGCAAATCATGGATAAATCCATGTCCA 2349
2401 AAAGAGACCAACCCTTGGTGACATGACTGGCAAATGCAAATCATGGATAAATCCATGTCCA 2460
636 AAAGAGACCAACCCTTGGTGACATGACTGGCAAATGCAAATCATGGATAAATCCATGTCCA 695

2350 GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC 2409
2461 GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC 2520
696 GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC 755

FIG. 2H

2410 CTCATCACCGTGAGGTCCAAGGCAAGAACCAAGTCGTCAATTGCTGCTGGAAGGAGTTCT 2469
2521 CTCATCACCGTGAGGTCCAAGGCAAGAACCAAGTCGTCAATTGCTGCTGGAAGGAGTTCT 2580
756 CTCATCACCGTGAGGTCCAAGGCAAGAACCAAGTCGTCAATTGCTGCTGGAAGGAGTTCT 815

2470 TTGGGAGCCCGACTCTCCGGGGCACTTCACGTCTATAGCCTTGGCTCAGATTGAAGATTT 2529
2581 TTGGGAGCCCGACTCTCCGGGGCACTTCACGTCTATAGCCTTGGCTCAGATTGAAGATTT 2640
816 TTGGGAGCCCGACTCTCCGGGGCACTTCACGTCTATAGCCTTGGCTCAGATTGAAGATTT 875

2530 CACTGCATTTCCCCACTCTGCCCCACCTCTCTCATGTGCTGAATCACATCCATGGTGAGCATT 2589
2641 CACTGCATTTCCCCACTCTGCCCCACCTCTCTCATGTGCTGAATCACATCCATGGTGAGCATT 2700
876 CACTGCATTTCCCCACTCTGCCCCACCTCTCTCATGTGCTGAATCACATCCATGGTGAGCATT 935

2590 TTGATGGACAAAGTGGCACATCCAGTGGAGCGGTGTAGATCCTGTATAGACATGGGGCTC 2649
2701 TTGATGGACAAAGTGGCACATCCAGTGGAGCGGTGTAGATCCTGTATAGACATGGGGCTC 2760
936 TTGATGGACAAAGTGGCACATCCAGTGGAGCGGTGTAGATCCTGTATAGACATGGGGCTC 995

2650 CTGGGA----- 2655
2761 CTGGGA----- 2766
996 CTGGGACAGTGAACCCGATCTGGTCATCGGCTCCCTTTTGCACCAGGTGGAGGAAGCA 1055

2656 -----GTAGAGAGACACACTAACAGCCACACCCCTCTG 2687
2767 -----GTAGAGAGACACACTAACAGCCACACCCCTCTG 2798
1056 GAAGGGAATTGTGGCTGCGTTTATTGAGTAGAGAGACACACTAACAGCCACACCCCTCTG 1115

FIG. 21

2688 GAAATCTGATACAGTAAATATATGACTGCACCAGAAATATGTGAAATAGCAGACATTCTG 2747
2799 GAAATCTGATACAGTAAATATATGACTGCACCAG----- 2833
1116 GAAATCTGATACAGTAAATATATGACTACACCAGAAATATGTGAAATAGCAGACATTCTG 1175

2748 CTTACTCATGTCCTTCCACAGTTTACTTCCTCGCTCCCTTTGCATCTAAACCTTTCTT 2807

1176 CTTACTCATGTCCTTCCACAGTTTACTTCCTCGCTCCCTTTGCATCTAAACCTTTCTT 1235

2808 CTTTCCCACTTATTGCCGTGTAGTCAGACCTGCTGTACAACCTATTTCCTCTTCCCTCTTG 2867

1236 CTTTCCCACTTATTGCCGTGTAGTC----- 1261

2868 AATGTCTTTCCAGTGGCTGGAAAGTCCCTCTGTGTTATCTGTTAGAACAGTCTCTGTA 2927

2928 CACAAATTCCTCTAAACATCCTTTTTTAAATAAGAAATTGTTTCAGCCATAAAGAAAGA 2987

2988 ACAAGATCATGCCCTTTGCAGGGACATGGATGGAGCTGGAGGCCATTATCCTTCATAAAC 3047

FIG. 2J

3048 TATTGCAGGAACAGAAAAACCAACTCCATATTCTCACTTGTAAGTGGGAGCTAAGTGA 3107

3108 GAACACGTGGACACATAGAGGGAAACAACACACACTGGGGCCCTATGAGAGGGCGGAAGGT 3167

3168 GGGAGGAGGAGAGATCAGGAAAAATAACTAATGGATACTTAGGGTGATGAAATAATCTG 3227

3228 TGTAACAAACCCCATGACACACCTTTATGTATGTAACAACAGCACTTCCTGCGCATG 3287

3288 TACCCCTGAACTTAAAAGTTAAAAAAGTTGAACTTAAAAATAACAGATTGGCCCATGC 3347

3348 CAATCAAAGTATAATAGAAAGCATAGTATAC 3378

FIG. 2K

FIG. 3A
FIG. 3B
FIG. 3C

FIG. 3

SEQ ID NO: 10

cDNA clone d3

MILLFQDSMSFIYKALERNIRTMFIGGSQLSQKHVSSPLASYFLSFPYARLGWAMTSADL
 NQDGHGDLVVGAPGYSRPGHIHIGRVYLIYGNDLGLPPVDLDDKEAHRILEGFQPSGRF
 GSALAVLDFNVDPDLAVGAPSVGSEQLTKGAVYVYFGSKQGMSSSPNITISCQDIYC
 NLGWTLLAADVNGDSEPDLVIGSPFAPGGGKQKGI VAAFYSGPSSLSDKEKLNVEAANWTV
 RGEEDFSWFGYSLHGVTVDNRTLLLVGSPTWKNASRLGHLLHIRDEKKS LGRVYGYFPPN
 GQSWFTISGDKAMGKLGTSLSGSHVLMNGTLKQVLLVGAPTYDDVSKVAFLT VTLHQGGA
 TRMYALISDAQPLLLSTFSGDRRFRFGGVLHLSDDLDDGLDEI IMAAPLRIADVTSGLI
 GGEDGRVYVYNGKETTLGDMTGKCKSWITPCPEEKAQYVLISPEASSRFGSSLI TVRSKA
 KNQVVIAAGRSSLGARLSGALHVYSLGSD

FIG. 3A

SEQ ID NO: 11

cDNA clone b2

MSAFRLWPGLLIMLGS LCHRGSPCGLSTHIEIGHRALEFLQLHNGRVNYRELLLEHQDAY
QAGIVFPDCFYPSICKGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDTTEKLVAFLF
GITSHMAADVSWHSLGLEQGLRTMGAIDFHGSYSEAHSAAGDFGDLVLSQFEFFNFNYLAR
RWYVPVKDLLGIYEKLYGRKVI TENVI VDCSHIQFLEMYGEMLA VSKLYPTYSTKSPFLV
EQFQEYFLGGLDDMAFWSTNIYHLTSEMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ
KNDFHRNLTTSLTESVDRNINITYTERGVFFSVNSWTPDSMSFIYKALERNIRTMFIGGSQL
SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY
GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDENVDGVPDLAVGAPSVGSEQLT
YKGAVVYVFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG
GKQKGI VAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTL LLLVGSP
TWKNASRLGHLLHIRDEKKS LGRVYGYFPPNGQSWFTISGDKAMGKLGTSLS SGHVL MNG
TLKQVLLVGAPTYDDVSKVAFLT VTLHQGGATRM YALISDAQPLLLSTFSGDRRFRS RFGG
VLHLSDDLDDGLDEI IMAAPLR IADVTSG LIGGEDGRVYVYNGKETTLGDMTGKCKSWIT
PCPEEKVSEKKKKK

FIG. 3B

SEQ ID NO: 12

cDNA clone a1

MSAFRLWPGLLIMLGSLCHRGSPCGLSTHIEIGHRALEFLQLHNGRVNYRELLLEHQDAY
QAGIVFPDCFYPSICKGGKFHDVSESTHWTPFLNASVHYIRENYPLPWEKDTTEKLVAFLF
GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQLFEFFNFNYLAR
RWYVPVKDLLGIYEKLYGRKVI TENVI VDCSHIQFLEM YGEMLA VSKLYPTYSTKSPFLV
EQFOEYFLGGLDDMAFWSTNIYHLTSFMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ
KNDFHRNLTTSLTESVDRNIN YTERGVFFSVNSWTPDMSFIYKALERNIRTMFIGGSQL
SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY
GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDFNVDPDLAVGAPSVGSEQLT
YKGAVVYVYFGSKQGMSSSPNITISQODIYCNLGTWTLAADVNGDSEPDLVIGSPFAPGG
GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTL LLVGSP
TWKNASRLGHLLHIRDEKKSLGRVYGYFFPPNGQSWFTISGDKAMGKLGTSLSSGHVLMNG
TLKQVLLVGAPTYDDVSKVAFLT VTLHQGGATRM YALISDAQPLLLSTFSGDRRFRSREGG
VLHLSDDLDDGLDEI IMAAPLRIADVTSGLIGGEDGRVYVYNGKETTLGDMTGKCKSWIT
PCPEEKAQYVLI SPEASSRFGSSLITVRSKAKNQV VIAAGRSSLGARLSGALHVYSLGSD

FIG. 3C

FIG. 4A
FIG. 4B
FIG. 4C

FIG. 4

SEQ ID NO: 13

19/41

2832 bp: 690 a 688 c 735 g 719 t

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1  gtgacctgct tagagagaag cggtaggtct gcacctggat ttggagtcc cagtctgct
61  gcagctctga gcattccac gtcaccagag aagccggtgg gcaatgagag catgtctgct
121  ttcaggttgt ggcctggcct gctgatcatg ttgggttctc tctgccatag aggttcaccg
181  tgtggccttt caacacacat agaaatagga cacagagctc tggagtcttc tcagcttcac
241  aatgggctg ttaactacag agagctgtta ctagaacacc aggatgcgta tcaggctgga
301  atcgtgttc ctgattgttt ttaccctagc atctgcaaag gaggaaaatt ccatgatgtg

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FIG. 4A

361 tctgagagca ctcactggac tccgtttctt aatgcaagcg ttcattatat ccgagagaac
421 tatccccttc cctgggagaa ggacacagag aaactggtag ctttcttggt tggattact
481 tctcacatgg cggcagatgt cagctggcat agtctgggcc ttgaacaagg attccttagg
541 accatgggag ctattgattt tcacggctcc tattcagagg ctcatcggc tggatgttt
601 ggaggagatg tgttgagcca gtttgaattt aattttaatt acctgcacg acgctggtat
661 gtgccagtca aagatctact gggaatttat gagaaactgt atggtcgaaa agtcattcacc
721 gaaaatgtaa tcgttgattg ttcacatata cagttcttag aatgtatgg tgagatgcta
781 gctgtttcca agttatatcc cacttactct acaaagtccc cgtttttggg ggaacaattc
841 caagagtatt ttcttggagg actggatgat atggcatttt ggtccactaa tatttaccat
901 ctaacaaagt tcatgttga gaatgggacc agtgactgca acctgcctga gaacctctg
961 ttcatgtcat gtggcgcca gcaaaaccac acccagggt caaaatgca gaaaatgat
1021 tttcacagaa atttgactac atccctaact gaaagtgttg acaggaatat aaactatact
1081 gaaagaggag tgttctttag tgtaaatcc tggaccccg gctctcagtt gtcacaaaag
1141 aaggctttgg aaaggaacat aaggacaatg ttcataagtg gctctcagtt gtcacaaaag
1201 cacgtctcca gcccttagc atctacttc ttgtcatttc cttatgcgag gcttggctgg
1261 gcaatgacct cagctgacct caaccaggat gggcacggtg acctcgtggg gggcgaccca
1321 ggctacagcc gccccggcca catccacatc gggcgctgtt acctcatcta cggcaatgac
1381 ctgggcctgc cacctgttga cctggacctg gacaaggagg ccacaggat ccttgaaggc
1441 ttccagccct caggtcgggt tggctcgcc ttggctgtgt tggactttaa cgtggacggc
1501 gtgcctgacc tggccgtggg agtccctcg gtgggctccg agcagctcac ctacaaagg
1561 gccgtgtatg tctactttgg ttccaaaaca ggaggaatgt cttcttcccc taacattcacc

FIG. 4B

1621 atttcttgcc aggacatcta ctgtaacttg ggctggactc tcttggctgc agatgtgaat
1681 ggagacagtg aaccgatctt ggtcatcggc tccccttttg caccaggtgg agggaaagcag
1741 aaggaattg tggctgcgtt ttattctggc ccagcctga gcgacaaaga aaaactgaac
1801 gtggaggcag ccaactggac ggtgagaggc gaggaagact tctcctggtt tggatatcc
1861 ctccacggtg tcaactgtgga caacagaacc ttgctgttgg ttgggagccc gacctggaag
1921 aatgccagca ggctgggcca ttgtttacac atccgagatg agaaaaagag ccttgggagg
1981 gtgtatggct acttcccacc aaacggccaa agctgggtta ccatttctgg agacaaaggca
2041 atggggaac tgggtacttc cctttccagt ggcacgtac tgatgaatgg gactctgaaa
2101 caagtgctgc tggttggagc ccctacgtac gatgacgtgt ctaagggtggc attcctgacc
2161 gtgaccctac accaaggcgg agccactcgc atgtacgcac tcatatctga cgcgcagcct
2221 ctgctgctca gcaccttcag cggagaccgc cgcttctccc gatttgggtg cgttctgcac
2281 ttgagtgacc tggatgatga tggcttagat gaaatcatca tggcagcccc cctgaggata
2341 gcagatgtaa cctctggact gattggggga gaagacggcc gagtatatgt atataatggc
2401 aaagagacca cccttgggtga catgactggc aaatgcaaat catggataac tccatgtcca
2461 gaagaaaagg cccaatatgt attgatctt cctgaagcca gctcaagggt tgggagctcc
2521 ctcatcaccg tgaggtccaa ggcaaaagaa caagtcgtca ttgctgctgg aaggagtctt
2581 ttgggagccc gactctccgg ggcacttcac gtctatagcc ttggctcaga ttgaagattt
2641 cactgcattt cccactctg cccacctctc tcatgctgaa tcacatccat ggtgagcatt
2701 ttgatggaca aagtggcaca tccagtggag cggtggtaga tcctgataga catggggctc
2761 ctgggagtag agagacacac taacagccac accctctgga aatctgatac agtaaatata
2821 tgactgcacc ag

FIG. 4C

2472 bp: 617 a 588 c 639 g 628 t

FIG. 5A

1 gtctgcacct ggatttttggg gtcccagtgc tgctgcagct ctgagcattc ccacgtcacc
61 agagaagccg gtgggcaatg agagcatgtc tgctttcagg ttgtggcctg gcctgctgat
121 catgttgggt tctctctgcc atagaggttc accgtgtggc ctttcaacac acatagaaat
181 aggacacaga gctctggagt ttcttcagct tcacaatggg cgtgtttaact acagagagct
241 gttactagaa caccaggatg cgtatcaggc tggaatcgtg ttctctgatt gtttttacc
301 tagcatctgc aaaggaggaa aattccatga tgtgtctgag agcactcact ggactccgtt
361 tcttaatgca agcgttcatt atatccgaga gaactatccc ctccctggg agaaggacac
421 agagaaactg gtgcttttct tgtttggaaat tacttctcac atggcggcag atgtcagctg
481 gcatagtctg ggccttgaac aaggattcct taggaccatg ggagctattg attttcacgg
541 ctctattca gaggctcatt cggctgggta ttttggagga gatgtgtga gccagtttga
601 atttaatttt aattaccttg cagcagctg gtatgtgcca gtcaaaagatc tactgggaat
661 ttatgagaaa ctgtatggtc gaaaagtcac caccgaaaat gtaatcgttg attgttcaca
721 tatccagttc ttagaaatgt atggtgagat gctagctgtt tccaagtta atcccactta
781 ctctacaaag tcccgtttt ttgtggaaca attccaagag tattttcttg gaggactgga
841 tgatatggca ttttgggtcca ctaatattha ccactaaca agcttcatgt tggagaatgg
901 gaccagtga ctgcaacctgc ctgagaacct tctgttcatt gcatgtggcg gccagcaaaa
961 ccacacccag ggctcaaaaa tgcagaaaaa tgattttcac agaaatttga ctacatccct
1021 aactgaaagt gttgacagga atataaacta tactgaaaga ggagtgttct ttagtgtaaa
1081 ttcctggacc cggattcca tgcctttat ctacaaggct ttggaaagga acataaggac

FIG. 5A

1141 aatgttcata ggtggctctc agttgtcaca aaagcacgtc tccagccctc tagcatctta
1201 cttcttgtca ttcccttatg cgaggcttgg ctgggcaatg acctcagctg acctcaacca
1261 ggatgggcac ggtgacctcg tggtagggcg accaggctac agccgccccg gccacatcca
1321 catcgggcgc gtgtacctca tctacggcaa tgacctgggc ctgccacctg ttgacctgga
1381 cctggacaag gaggcccaca ggatcccttga aggttccag ccctcaggtc ggtttggctc
1441 ggccttggct gtgttggact ttaacgtgga cggcgtgcct gacctggccg tgggagctcc
1501 ctcggtgggc tccgagcagc tcacctacaa aggtgccgtg tatgtctact ttggttccaa
1561 acaaggagga atgtcttctt cccctaacat caccatttct tgccaggaca tctactgtaa
1621 cttgggctgg actctcttgg ctgcagatgt gaatggagac agtgaaccg atctggtcat
1681 cggctcccct ttgcaccag gtggaggga gcagaaggga attgtggctg cgttttattc
1741 tggccccagc ctgagcgaca aagaaaaact gaacgtggag gcagccaact ggacggtgag
1801 aggcgaggaa gacttctcct ggtttggata ttcccttcac ggtgtcactg tggacaacag
1861 aaccttgctg ttggttggga gcccgacctg gaagaatgcc agcaggctgg gccatttgtt
1921 acacatccga gatgagaaaa agagccttgg gaggtgtat ggctacttcc caccaaacgg
1981 ccaaagctgg ttaccattt ctggagacaa ggcaatgggg aaactgggta ctcccttctc
2041 cagtggccac gtactgatga atgggactct gaaacaagtg ctgctgggtg gagccccctac
2101 gtacgatgac gtgtctaagg tggcattcct gaccgtgacc ctacaccaag gcggagccac
2161 tcgcatgtac gactcatat ctgacgcgca gcctctgctg ctcagcacct tcagcggaga
2221 ccgccgcttc tccgatttg gtggcgttct gcaattgagt gacctggatg atgatggctt
2281 agatgaaatc atcatggcag cccccctgag gatagcagat gtaacctctg gactgattgg
2341 gggagaagac ggccgagtat atgtatataa tggcaaaagag accacccttg gtgacatgac
2401 tggcaaatgc aaatcatgga taactccatg tccagaagaa aaggtaatg aaaaaaaaaa
2461 aaaaaaaaaa aa

FIG. 5B

FIG. 6A
FIG. 6B

FIG. 6A

SEQ ID NO: 15

1942 bp: 455 a 496 c 502 g 489 t

FIG. 6

1 gggctgtaac tctgccatcc ctacagcataa ttggggggta tgatttcact atcctaattg
61 cctgtccctaa gtgattccttac ttgctgatatg gacctaatgt ttatatattat tgttttagcac
121 ttctaaaaaac tcatttcctt tacacaaagtc caatactttg gacaggaaac agtagctttg
181 ttgattatgc tacgtgtctt tactgtctat aatgattcctt ttatttcagg attccatgtc
241 ctttatctac aaggctttgg aaaggaaacat aaggacaatg ttcataggtg gctctcagtt
301 gtcacaaaag cacgtctcca gcccttagc atcttacttc ttgtcatttc cttatgcgag
361 gcttggctgg gcaatgacct cagctgacct caaccaggat gggcacggtg acctcgtggt
421 gggcgcacca ggctacagcc gccccggcca catccacatc gggcgctgt acctcatcta
481 cggcaatgac ctgggcctgc cacctgttga cctggacctg gacaaggagg cccacaggat
541 ccttgaaggc ttccagccct caggtcggtt tggctcggcc ttggctgtgt tggactttaa
601 cgtggacggc gtgcctgacc tggccgtggg agctccctcg gtgggctccg agcagctcac
661 ctacaaaagg gccgtgtatg tctactttgg ttccaaacaa ggagggaatgt ctcttcccc
721 taacatcacc atttcttgcc aggacatcta ctgtaacttg ggctggactc tcttggctgc

781 agatgtgaat ggagacagtg aaccgatct ggtcatcggc tccccttttg caccaggtgg
841 agggaaagcag aagggaattg tggctgcgtt ttattctggc ccagcctga gcgacaaaga
901 aaaactgaac gtggaggcag ccaactggac ggtgagaggc gaggaagact tctcctggtt
961 tggatatcc cttcacggtg tcaactgtgga caacagaacc ttgctgttgg ttgggagccc
1021 gacctggaag aatgccagca ggctgggcca tttgttacac atccgagatg agaaaaagag
1081 ccttgggagg gtgtatggct acttcccacc aaacggccaa agctggttta ccatttctgg
1141 agacaaaggca atggggaac tgggtacttc cctttccagt ggccacgtac tgatgaatgg
1201 gactctgaaa caagtgtgc tggttggagc cctacgtac gatgacgtgt ctaagggtggc
1261 attcctgacc gtgacctac accaaggcgg agccactcgc atgtacgcac tcatatctga
1321 cgcgcagcct ctgctgctca gcaccttcag cggagaccgc cgcttctccc gatttgggtgg
1381 cgttctgcac ttgagtgacc tggatgatga tggcttagat gaaatcatca tggcagcccc
1441 cctgaggata gcagatgtaa cctctggact gattgggga gaagacggcc gagtatatgt
1501 atataatggc aaagagacca cccttgggtga catgactggc aaatgcaaat catggataac
1561 tccatgtcca gaagaaaagg cccaatatgt attgatttct cctgaagcca gctcaagggtt
1621 tgggagctcc ctcatcacccg tgagggtccaa ggcaaaagaa caagtcgtca ttgctgctgg
1681 aaggagtctt ttgggagccc gactctccgg ggcacttcac gtctatagcc ttggctcaga
1741 ttgaagattt cactgcattt cccactctg cccacctctc tcatgctgaa tcacatccat
1801 ggtgagcatt ttgatggaca aagtggcaca tccagtggag cggtaggtaga tcctgataga
1861 catggggctc ctgggagtag agagacacac taacagccac accctctgga aatctgatac
1921 agtaaatata tgactgcacc ag

FIG. 6B

SEQ ID NO: 16	database	MSAFRLWPGLLIMLGSLCHRGSPCGLSTHVEIGHRALEFLQLHNGRVNYRELLLEHQDAY	60
SEQ ID NO: 17	d3	-----	
SEQ ID NO: 18	b2	MSAFRLWPGLLIMLGSLCHRGSPCGLSTHVEIGHRALEFLQLHNGRVNYRELLLEHQDAY	60
SEQ ID NO: 19	a1	MSAFRLWPGLLIMLGSLCHRGSPCGLSTHVEIGHRALEFLQLHNGRVNYRELLLEHQDAY	60
	database	QAGIVFPDCFYPSICKGKGFHDVSESTHWTFFLNASVHYIRENYPLPWEKDTKLVAFLE	120
	d3	-----	
	b2	QAGIVFPDCFYPSICKGKGFHDVSESTHWTFFLNASVHYIRENYPLPWEKDTKLVAFLE	120
	a1	QAGIVFPDCFYPSICKGKGFHDVSESTHWTFFLNASVHYIRENYPLPWEKDTKLVAFLE	120
	database	GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQFEFNFNYLAR	180
	d3	-----	
	b2	GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQFEFNFNYLAR	180
	a1	GITSHMAADVSWHSLGLEQGFRLRTMGAIDFHGSYSEAHSAAGDFGGDVLSQFEFNFNYLAR	180
	database	RWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFLV	240
	d3	-----	
	b2	RWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFLV	240
	a1	RWYVPVKDLLGIYEKLYGRKVIITENVIVDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFLV	240
	database	EQFQEYFLGGLDDMAFWSTNIYHLTIFMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ	300
	d3	-----	
	b2	EQFQEYFLGGLDDMAFWSTNIYHLTIFMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ	300
	a1	EQFQEYFLGGLDDMAFWSTNIYHLTIFMLENGTSDCNLPENPLFIACGGQQNHTQGSKMQ	300

FIG. 7A
FIG. 7B
FIG. 7C

FIG. 7A

FIG. 7

database	KNDFHRNLTTSLTESVDRNININITERGVFFSVNSWTPDMSFSIYKALERNIRTMFIGGSQ	360
d3	-----MILLFQDSMSFSIYKALERNIRTMFIGGSQ	30
b2	KNDFHRNLTTSLTESVDRNININITERGVFFSVNSWTPDMSFSIYKALERNIRTMFIGGSQ	360
a1	KNDFHRNLTTSLTESVDRNININITERGVFFSVNSWTPDMSFSIYKALERNIRTMFIGGSQ	360
database	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	420
d3	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	90
b2	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	420
a1	SQKHVSSPLASYFLSFPYARLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIY	420
database	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDENVDGVPDЛАVGA PSVGSEQLT	480
d3	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDENVDGVPDЛАVGA PSVGSEQLT	150
b2	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDENVDGVPDЛАVGA PSVGSEQLT	480
a1	GNDLGLPPVDLDDKEAHRILEGFQPSGRFGSALAVLDENVDGVPDЛАVGA PSVGSEQLT	480
database	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	540
d3	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	210
b2	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	540
a1	YKGAVVYVYFGSKQGMSSSPNITISCQDIYCNLGTLLAADVNGDSEPDLVIGSPFAPGG	540
database	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	600
d3	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	270
b2	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	600
a1	GKQKGIVAAFYSGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTLLLVGSP	600

FIG. 7B

database	TKKNASRLGHLHLHIRDEKKS LGRVYGYFPNPGQSWFTISGDKAMGKLGTSLSGHVLMNG	660
d3	TKKNASRLGHLHLHIRDEKKS LGRVYGYFPNPGQSWFTISGDKAMGKLGTSLSGHVLMNG	330
b2	TKKNASRLGHLHLHIRDEKKS LGRVYGYFPNPGQSWFTISGDKAMGKLGTSLSGHVLMNG	660
a1	TKKNASRLGHLHLHIRDEKKS LGRVYGYFPNPGQSWFTISGDKAMGKLGTSLSGHVLMNG	660
database	TLKQVLLVGAPTYDDVSKVAFLTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	720
d3	TLKQVLLVGAPTYDDVSKVAFLTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	390
b2	TLKQVLLVGAPTYDDVSKVAFLTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	720
a1	TLKQVLLVGAPTYDDVSKVAFLTVTLHQGGATRM YALISDAQPLLLSTFSGDRRFSRFGG	720
database	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKCKSWIT	780
d3	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKCKSWIT	450
b2	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKCKSWIT	780
a1	VLHLSDLDDGLDEI IMAAPLRIADVTSLIGGEDGRVYVYNGKETTLGDMTGKCKSWIT	780
database	PCPEEKAQYVVLISPEASSRFGSSLI TVRSKAKNQV VIAAGRSSLGALHVYSLGSD	840
d3	PCPEEKAQYVVLISPEASSRFGSSLI TVRSKAKNQV VIAAGRSSLGALHVYSLGSD	510
b2	PCPEEKVSEKKKKK-----	795
a1	PCPEEKAQYVVLISPEASSRFGSSLI TVRSKAKNQV VIAAGRSSLGALHVYSLGSD	840
Database	840 aa	
d3	510 aa	
b2	795 aa	
a1	840 aa	

FIG. 7C

FIG. 8A
FIG. 8B
FIG. 8C
FIG. 8D
FIG. 8E
FIG. 8F
FIG. 8G
FIG. 8H
FIG. 8I
FIG. 8J
FIG. 8K
FIG. 8L

FIG. 8

1: pancreatic-form: cDNA sequence from GenBank database (L11702) SEQ ID NO:20
2: cDNA clone A1 SEQ ID NO:21
3: cDNA clone B2 SEQ ID NO:22
4: cDNA clone D3 SEQ ID NO:23

```
-----  
1  GTGACCTGCTTAGAGAGAGCGGTGGTCTGCACCTGGATTTTGGAGTCCCAGTGTGCT 60  
1  -----GTCCTGCACCTGGATTTTGGAGTCCCAGTGTGCT 34  
-----  
1  -----ATGTCTGCT 9  
61  GCAGCTCTGAGCATCCACGTCACAGAGAAGCCGGTGGCAATGAGAGCATGTCTGCT 120  
35  GCAGCTCTGAGCATCCACGTCACAGAGAAGCCGGTGGCAATGAGAGCATGTCTGCT 94  
-----  
10  TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTGCCATAGAGGTTACCCG 69  
121  TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTGCCATAGAGGTTACCCG 180  
95  TTCAGGTTGTGGCCTGGCCTGCTGATCATGTTGGGTTCTCTGCCATAGAGGTTACCCG 154  
-----  
70  TGTGGCCTTTCAACACACAGTAGAAATAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 129  
181  TGTGGCCTTTCAACACACACATAGAAATAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 240  
155  TGTGGCCTTTCAACACACATAGAAATAGGACACAGAGCTCTGGAGTTTCTTCAGCTTCAC 214  
-----
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FIG. 8A

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130	AATGGCGGTGTTAACTACAGAGAGCTGTTACTAGAAACACCAGGATGCGTATCAGGCTGGA	189
241	AATGGCGGTGTTAACTACAGAGAGCTGTTACTAGAAACACCAGGATGCGTATCAGGCTGGA	300
215	AATGGCGGTGTTAACTACAGAGAGCTGTTACTAGAAACACCAGGATGCGTATCAGGCTGGA	274

190	ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAAGGAGGAAAAATTCATGATGTG	249
301	ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAAGGAGGAAAAATTCATGATGTG	360
275	ATCGTGTTTCCTGATTGTTTTTACCCTAGCATCTGCAAAGGAGGAAAAATTCATGATGTG	334

250	TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC	309
361	TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC	420
335	TCTGAGAGCACTCACTGGACTCCGTTTCTTAATGCAAGCGTTCATTATATCCGAGAGAAC	394

310	TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTCTTGTGGAATTACT	369
421	TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTCTTGTGGAATTACT	480
395	TATCCCCCTTCCCTGGGAGAGGACACAGAGAAACTGGTAGCTTCTTGTGGAATTACT	454

370	TCTCACATGGCGGCAGATGTCAGCTGGCATAAGTCTGGGCCCTTGAACAAGGATTCCTTAGG	429
481	TCTCACATGGCGGCAGATGTCAGCTGGCATAAGTCTGGGCCCTTGAACAAGGATTCCTTAGG	540
541	TCTCACATGGCGGCAGATGTCAGCTGGCATAAGTCTGGGCCCTTGAACAAGGATTCCTTAGG	514

FIG. 8B

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430  ACCATGGGAGCTATTGATTTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 489
541  ACCATGGGAGCTATTGATTTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 600
515  ACCATGGGAGCTATTGATTTTTCACGGCTCCTATTTCAGAGGCTCATTCGGCTGGTGATTTT 574
-----

490  GGAGGAGATGTGTGAGCCAGTTTGAATTTTAATTTTAAATTACCTTGACGACGCTGGTAT 549
601  GGAGGAGATGTGTGAGCCAGTTTGAATTTTAATTTTAAATTACCTTGACGACGCTGGTAT 660
575  GGAGGAGATGTGTGAGCCAGTTTGAATTTTAATTTTAAATTACCTTGACGACGCTGGTAT 634
-----

550  GTGCCAGTCAAAGATCTACTGGGAATTTATGAGAAACTGTATGGTCGAAAAGTCATCACC 609
661  GTGCCAGTCAAAGATCTACTGGGAATTTATGAGAAACTGTATGGTCGAAAAGTCATCACC 720
635  GTGCCAGTCAAAGATCTACTGGGAATTTATGAGAAACTGTATGGTCGAAAAGTCATCACC 694
-----

610  GAAAATGTAATCGTTGATTGTTACATATCCAGTTCTTAGAAAATGTATGGTGAGATGCTA 669
721  GAAAATGTAATCGTTGATTGTTACATATCCAGTTCTTAGAAAATGTATGGTGAGATGCTA 780
695  GAAAATGTAATCGTTGATTGTTACATATCCAGTTCTTAGAAAATGTATGGTGAGATGCTA 754
-----

670  GCTGTTTCCAAGTTATATATCCCACTTACTCTACAAAGTCCCCGTTTTTTGGTGGAACAATTC 729
781  GCTGTTTCCAAGTTATATATCCCACTTACTCTACAAAGTCCCCGTTTTTTGGTGGAACAATTC 840
755  GCTGTTTCCAAGTTATATATCCCACTTACTCTACAAAGTCCCCGTTTTTTGGTGGAACAATTC 814
-----

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FIG. 8C

730	CAAGAGTATTTTCTTGGAGGACTGGATGATATGGCATTTTGGTCCACTAATAATTTACCAT	789
841	CAAGAGTATTTTCTTGGAGGACTGGATGATATGGCATTTTGGTCCACTAATAATTTACCAT	900
815	CAAGAGTATTTTCTTGGAGGACTGGATGATATGGCATTTTGGTCCACTAATAATTTACCAT	874
	-----GGGCTGTAAC	10
790	CTAACAAATCTTCATGTTGGAGAAATGGGACCAGTGACTGCAACCTGCCCTGAGAACCCCTCTG	849
901	CTAACAAAGCTTCATGTTGGAGAAATGGGACCAGTGACTGCAACCTGCCCTGAGAACCCCTCTG	960
875	CTAACAAAGCTTCATGTTGGAGAAATGGGACCAGTGACTGCAACCTGCCCTGAGAACCCCTCTG	934
11	TCTGCCATCCCTCAGCATAAATTTGGGGGTATGATTTTCACTATCCTAATTGCCCTGTCCCTAA	70
850	TTTCATTGTCATGTGGCGGCCAGCAAAACCAACCCAGGGCTCAAAAATGCAGAAAAATGAT	909
961	TTTCATTGTCATGTGGCGGCCAGCAAAACCAACCCAGGGCTCAAAAATGCAGAAAAATGAT	1020
935	TTTCATTGTCATGTGGCGGCCAGCAAAACCAACCCAGGGCTCAAAAATGCAGAAAAATGAT	994
71	GTGATCCTTACTTGCTGATAGGACCCTAAATGTTTATTTATTGTTTAGCACCTTCTCTAAAAAC	130
910	TTTCACACAGAAATTTGACTACATCCCTAACTGAAAGTGTGACAGGAAATATAAACTATACT	969
1021	TTTCACACAGAAATTTGACTACATCCCTAACTGAAAGTGTGACAGGAAATATAAACTATACT	1080
995	TTTCACACAGAAATTTGACTACATCCCTAACTGAAAGTGTGACAGGAAATATAAACTATACT	1054
131	TCATTTCCCTTTACACAAGTCCAATACTTTGGACAGGAAACAGTAGCTTTGTTGATTATGC	180
970	GAAAGAGGAGTGTTCTTTAGTGTAATAATTCCTGGACCCCGGATTCCCATGTCCCTTTATCTAC	1029
1081	GAAAGAGGAGTGTTCTTTAGTGTAATAATTCCTGGACCCCGGATTCCCATGTCCCTTTATCTAC	1140
1055	GAAAGAGGAGTGTTCTTTAGTGTAATAATTCCTGGACCCCGGATTCCCATGTCCCTTTATCTAC	1114
181	TACGTGCTTTACTGCTATAATGATTCCTTTTATTTCAGGATTCCCATGTCCCTTTATCTAC	240

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FIG. 8D

1030 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1089
1141 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1200
1115 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 1174
241 AAGGCTTTGGAAGGAACATAAGGACAAATGTTCATAGGTGGCTCTCAGTTGTCACAAAG 300

1090 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCTTATGCGAGGCTTGGCTGG 1149
1201 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCTTATGCGAGGCTTGGCTGG 1260
1175 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCTTATGCGAGGCTTGGCTGG 1234
301 CACGTCTCCAGCCCCCTTAGCATCTTACTTCTTGTCATTTCCTTATGCGAGGCTTGGCTGG 360

1150 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 1209
1261 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 1320
1235 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 1294
361 GCAATGACCTCAGCTGACCTCAACCAGGATGGGCACGGTGACCTCGTGGTGGCGCACCA 420

1210 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1269
1321 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1380
1295 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 1354
421 GGCTACAGCCGCCCGGCCACATCCACATCGGGCGCGTGACCTCATCTACGGCAATGAC 480

1270 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 1329
1381 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 1440
1355 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 1414
481 CTGGGCCCTGCCACCTGTTGACCTGGACCTGGACAAGGAGGCCCAACAGGATCCTTGAAGGC 540

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FIG. 8E

1330 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 1389
1441 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 1500
1415 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 1474
541 TTCCAGCCCTCAGGTCGGTTTGGCTCGGCCCTTGGCTGTGTTGGACTTTAAACGTGGACGGC 600

1390 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1449
1501 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1560
1475 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 1534
601 GTGCCTGACCTGGCCGTGGAGCTCCCTCGGTGGGCTCCGAGCAGCTCACCTACAAAGGT 660

1450 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 1509
1561 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 1620
1535 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 1594
661 GCCGTGATGTCTACTTTGGTTCCAAACAAGAGGAATGTCTTCTTCCCCCTAACATCACC 720

1510 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1569
1621 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1680
1595 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 1654
721 ATTTCTTGCCAGGACATCTACTGTAACTTGGCTGGACTCTCTTGGCTGCAGATGTGAAT 780

1570 GGAGACAGTGAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 1629
1681 GGAGACAGTGAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 1740
1655 GGAGACAGTGAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 1714
781 GGAGACAGTGAACCCGATCTGGTCATCGGCTCCCCCTTTTGCAACCAGGTGGAGGGAAGCAG 840

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FIG. 8F

1630 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 1689
1741 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 1800
1715 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 1774
841 AAGGGAATTGTGGCTGCGTTTATTCTGGCCCCAGCCTGAGCGACAAAGAAAACCTGAAC 900
1690 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 1749
1801 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 1860
1775 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 1834
901 GTGGAGGCAGCCAACTGGACGGTGAGAGGCGAGGAAGACTTCTCCTGGTTTGGATATTCC 960
1750 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTGTGGTGGAGCCCCGACCTGGAAG 1809
1861 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTGTGGTGGAGCCCCGACCTGGAAG 1920
1835 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTGTGGTGGAGCCCCGACCTGGAAG 1894
961 CTTACCGGTGTCACTGTGGACAACAGAAACCTTGCTGTGTGGTGGAGCCCCGACCTGGAAG 1020
1810 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1869
1921 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1980
1895 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1954
1021 AATGCCAGCAGGCTGGGCCATTGTGTACACATCCGAGATGAGAAAGAGCCTTGGGAGG 1080
1870 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 1929
1981 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 2040
1955 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 2014
1081 GTGTATGGCTACTTCCCAACCAACGGCCAAAGCTGGTTTACCATTTCTGGAGACAAGGCA 1140

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FIG. 8G

1930 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 1989
2041 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 2100
2015 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 2074
1141 ATGGGGAAACTGGGTACTTCCCTTTCCAGTGGCCACGTACTGATGAATGGGACTCTGAAA 1200
1990 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 2049
2101 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 2160
2075 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 2134
1201 CAAGTGCTGCTGGTTGGAGCCCCCTACGTACGATGACGTGTCTAAGGTGGCATTCCTGACC 1260
2050 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATCTGACGCGCAGCCT 2109
2161 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATCTGACGCGCAGCCT 2220
2135 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATCTGACGCGCAGCCT 2194
1261 GTGACCCCTACACCAAGGCGGAGCCACTCGCATGTACGCACTCATATCTGACGCGCAGCCT 1320
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2110 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 2169
2221 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 2280
2195 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 2254
1321 CTGCTGCTCAGCACCTTCAGCGGAGACCGCCGCTTCTCCCGATTGTTGGTGGCGTTCTGCAC 1380
2170 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATATGGCAGCCCCCTGAGGATA 2229
2281 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATATGGCAGCCCCCTGAGGATA 2340
2255 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATATGGCAGCCCCCTGAGGATA 2314
1381 TTGAGTGACCTGGATGATGATGGCTTAGATGAAATCATATGGCAGCCCCCTGAGGATA 1440

FIG. 8H

2230	GCAGATGTAACCTCTGGACTGTGTTGGGGAGAAGACGGCCGAGTATATGTATAAATGGC	2289
2341	GCAGATGTAACCTCTGGACTGTGTTGGGGAGAAGACGGCCGAGTATATGTATAAATGGC	2400
2315	GCAGATGTAACCTCTGGACTGTGTTGGGGAGAAGACGGCCGAGTATATGTATAAATGGC	2374
1441	GCAGATGTAACCTCTGGACTGTGTTGGGGAGAAGACGGCCGAGTATATGTATAAATGGC	1500
2290	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAACTCCATGTCCA	2349
2401	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAACTCCATGTCCA	2460
2375	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAACTCCATGTCCA	2434
1501	AAAGAGACCACCCCTTGTTGACATGACTGGCAAATGCAAAATCATGGATAACTCCATGTCCA	1560
2350	GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC	2409
2461	GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC	2520
2435	GAAGAAAAGGTAAGTGAAAAAAA AAA AAAAAAAAA-----	2472
1561	GAAGAAAAGGCCCAATATGTATTGATTTCTCCTGAAGCCAGCTCAAGGTTTGGGAGCTCC	1620
2410	CTCATCACCGTGAGGTCCAAGGCCAAAGAACCAAGTCGTCA TTGCTGCTGGAAGGAGTTCT	2469
2521	CTCATCACCGTGAGGTCCAAGGCCAAAGAACCAAGTCGTCA TTGCTGCTGGAAGGAGTTCT	2580

1621	CTCATCACCGTGAGGTCCAAGGCCAAAGAACCAAGTCGTCA TTGCTGCTGGAAGGAGTTCT	1680
2470	TTGGGAGCCCCGACTCTCCGGGGCACTTCACGTCTATAGCCCTTGGCTCAGATTGAAGATTT	2529
2581	TTGGGAGCCCCGACTCTCCGGGGCACTTCACGTCTATAGCCCTTGGCTCAGATTGAAGATTT	2640

1681	TTGGGAGCCCCGACTCTCCGGGGCACTTCACGTCTATAGCCCTTGGCTCAGATTGAAGATTT	1740

Fig. 8

2530	CACTGCATTTC	2589
2641	CACTGCATTTC	2700

1741	CACTGCATTTC	1800
2590	TTGATGGACAA	2649
2701	TTGATGGACAA	2760

1801	TTGATGGACAA	1860
2650	CTGGGAGTAGA	2709
2761	CTGGGAGTAGA	2820

1861	CTGGGAGTAGA	1920
2710	TGACTGCACCA	2769
2821	TGACTGCACCA	2880

1921	TGACTGCACCA	1952

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Fig. 8

2770 GTTACTTCCTCGCTCCCTTTGCACTCTAAACCTTTCTTCTTTCCCAACTTATTGCCTGTA 2829
2881 AAAAAAAAAAAAAAAAAAAAAAAAAA----- 2915

2830 GTCAGACCTGCTGTACAACCTATTTCCTCTCTTGAATGTCTTCCAGTGGCTGGAA 2889

2890 AGTCCCCTCTGTGTTATCTGTAGAACAGTCTCTGTACACAATTCTCTCTAAACATC 2949

2950 CTTTTTAAAAAGAAATTGTTTCAGCCATAAAGAAAGAACAGATCATGCCCTTTGCAGG 3009

3010 GACATGGATGGAGCTGGAGGCCATTATCCTTCATAAACTATTGCAGGAACAGAAACCAA 3069

3070 AACTCCATATTCTCACTTGTAAGTGGAGCTAAGTGAGAACACGTGGACACATAGAGGG 3129

3130 AAACAACACACTGGGGCCTATGAGAGGGCGGAAGGTGGAGGAGAGATCAGGAA 3189

3190 AAATAACTAATGGATACTTAGGGTGATGAAATAATCTGTGTAACAAACCCCATGACACA 3249

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3250 CCTTTATGTATGTAACAACCAGCACTTCCTGCGCATGTACCCCTGAACTTAAAGTTAA 3309

3310 AAAAAGTTGAACCTTAAAAATAACAGATTGGCCCATGCCAATCAAAGTATAATAGAAAGC 3369

3370 ATAGTATAC 3378

FIG. 8L